SEQUENCE LISTING

<110> Kunsch et al

<120> Human Hepatoma-Derived Growth Factor-2

<130> PF198D1C1

<140> Unassigned
<141> 2001-11-15

<150> 09/263,625
<151> 1999-03-05

<150> 08/464,600
<151> 1995-06-05

<160> 7

<170> PatentIn version 3.1

<210> 1
<211> 3202
<212> DNA
<213> human

<220>
<221> CDS
<222> (34)..(780)
<223>

<400> 1

```
gaattcgtgc tcttagggtg gttgggtggt aag atg gcg gct gtg agt ctg cgg      54
                                      Met Ala Ala Val Ser Leu Arg
                                      1               5

ctc ggc gac ttg gtg tgg ggg aaa ctc ggc cga tat cct cct tgg cca      102
Leu Gly Asp Leu Val Trp Gly Lys Leu Gly Arg Tyr Pro Pro Trp Pro
        10                  15                  20

gga aag att gtt aat cca cca aag gac ttg aag aaa cct cgc gga aag      150
Gly Lys Ile Val Asn Pro Pro Lys Asp Leu Lys Lys Pro Arg Gly Lys
    25                  30                  35

aaa tgc ttc ttt gtg aaa ttt ttt gga aca gaa gat cat gcc tgg atc      198
Lys Cys Phe Phe Val Lys Phe Phe Gly Thr Glu Asp His Ala Trp Ile
40                  45                  50                  55

aaa gtg gaa cag ctg aag cca tat cat gct cat aaa gag gaa atg ata      246
Lys Val Glu Gln Leu Lys Pro Tyr His Ala His Lys Glu Glu Met Ile
                60                  65                  70

aaa att aac aag ggt aaa cga ttc cag caa gcg gta gat gct gtc gaa      294
Lys Ile Asn Lys Gly Lys Arg Phe Gln Gln Ala Val Asp Ala Val Glu
            75                  80                  85

gag ttc ctc agg aga gcc aaa ggg aaa gac cag acg tca tcc cac aat      342
Glu Phe Leu Arg Arg Ala Lys Gly Lys Asp Gln Thr Ser Ser His Asn
        90                  95                  100
```

```
tct tct gat gac aag aat cga cgt aat tcc agt gag gag aga agt agg       390
Ser Ser Asp Asp Lys Asn Arg Arg Asn Ser Ser Glu Glu Arg Ser Arg
    105                 110                 115

cca aac tca ggt gat gag aag cgc aaa ctt agc ctg tct gaa ggg aag       438
Pro Asn Ser Gly Asp Glu Lys Arg Lys Leu Ser Leu Ser Glu Gly Lys
120                 125                 130                 135

gtg aag aag aac atg gga gaa gga aag aag agg gtg tct tca ggc tct       486
Val Lys Lys Asn Met Gly Glu Gly Lys Lys Arg Val Ser Ser Gly Ser
                140                 145                 150

tca gag aga ggc tcc aaa tcc cct ctg aaa aga gcc caa gag caa agt       534
Ser Glu Arg Gly Ser Lys Ser Pro Leu Lys Arg Ala Gln Glu Gln Ser
            155                 160                 165

ccc cgg aag cgg ggt cgg ccc cca aag gat gag aag gat ctc acc atc       582
Pro Arg Lys Arg Gly Arg Pro Pro Lys Asp Glu Lys Asp Leu Thr Ile
        170                 175                 180

ccg gag tct agt acc gtg aag ggg atg atg gcc gga ccg atg gcc gcg       630
Pro Glu Ser Ser Thr Val Lys Gly Met Met Ala Gly Pro Met Ala Ala
    185                 190                 195

ttt aaa tgg cag cca acc gca agc gag cct gtt aaa gat gca gat cct       678
Phe Lys Trp Gln Pro Thr Ala Ser Glu Pro Val Lys Asp Ala Asp Pro
200                 205                 210                 215

cat ttc cat cat ttc ctg cta agc caa aca gag aag cca gct gtc tgt       726
His Phe His His Phe Leu Leu Ser Gln Thr Glu Lys Pro Ala Val Cys
                220                 225                 230

tac cag gca atc acg aag aag ttg aaa ata tgt gaa gac ctc ctt ctt       774
Tyr Gln Ala Ile Thr Lys Lys Leu Lys Ile Cys Glu Asp Leu Leu Leu
            235                 240                 245

cct agg tgaagtgggc aatgcagcca agatgatgct gatcgtgaac atggtccaag        830
Pro Arg

ggagcttcat ggccactatt gccgaggggc tgaccctggc ccaggtgaca ggccagtccc     890

agcagacact cttggacatc ctcaatcagg gacagttggc cagcatcttc ctggaccaga     950

agtgccaaaa tatcctgcaa ggaaacttta agcctgattt ctacctgaaa tacattcaga    1010

aggatctccg cttagccatt gcgctgggtg atgcggtcaa ccatccgact cccatggcag    1070

ctgcagcaaa tgaggtgtac aaaagagcca aggcgctgga ccagtctgac aacgatatgt    1130

ccgccgtgta ccgagcctac atacactaag ctgtcgacac cccgccctca cccctccaat    1190

ccccccctctg acccccctctt cctcacatgg ggtcgggggc ctgggagttc attctggtac    1250

cagcccacct atctccattt ccttttatac agactttgag acttgccatc agcacagcac    1310

acagcagcac ccttcccctg aggtcggtgg ggaggggaca agtgtcagca ggattggcgt    1370

gtgggaaagc tcttgagctg ggcactggcc ccccggacga ggtggytgtg tgttcacaca    1430

cacacacaca cacacacaca cacacacaca cacaggctct cgcccccagga tagaagctgc    1490
```

ccagaaactg ctgcctggct ttttttcttc cgagcttgtc ttatctcaaa ccccttccag 1550

tcaaggaact agaatcagca acgagagttg gaagccttcc cacagcttcc cccagagcga 1610

agaggctgta gtcatgtccc catcccccac tggattccct acaaggagag gccttgggcc 1670

cagatgagcc agtacagact ccagacagag gggcccttgg ggccctccaa cctcaggtga 1730

tgagctgaga aagatgttca cgtctaagcg tccagtgtgc acccagcgct ccatagacgc 1790

ctttgtgaac tgaaaagaga ctggcagagt cccgagaaga tggggccctg gctttccagg 1850

gagtgcagca agcagccggc ctgcaggtga gcatggaggc ccggccctca ccgcctcgaa 1910

gccatgcccc agatgccact gccacagcgg gcgctcgctc ctccctaggc tgttttagta 1970

tttggatttg cattccatcc cttgggaggg agtcctcagg gccactagtg atgagccaag 2030

aggagtgggg gttgggggcg ctcctttctg tttccgttag gccacagact cttcacctgg 2090

ctctgactta cctcggtccc ctcccagtgg tcccaccttc tccaccctgc cctgccaagt 2150

cccctgcatg cccaccgctc tccatcctcc ctcctctccc tcttcctccc gtggagacag 2210

tatttctttc tgtctgtccc tttggcccag acccagcctg accaacgatg agcatttctt 2270

aggctcagct cttgatacgg aaacgagtgt cttcactcca gccagcatca tggtcttcgg 2330

tgcttcccgg gcccggggtc tgtcgggagg gaagagaact gggcctgacc tacctgaact 2390

gactggccct ccgaggtggg tctgggacat cctagaggcc ctacatttgt ccttggatag 2450

gggaccgggg ggggcttgga atgttscaaa aaaaaaagtt acccaaggga tgtcagtttt 2510

ttatccctct gcatgggttg gattttccaa aatcataatt tgcagaagga aggccagcat 2570

ttacgatgca atatgtaatt atatataggg tggccacact agggcggggt ccttcccccc 2630

tcacagcttt ggcccctttc agagattaga aactgggtta gaggattgca gaagacgagt 2690

gggggggaggg cagggaagat gcctgtcggg tttttagcac agttcatttc actgggattt 2750

tgaagcattt ctgtctgaac acaaagcctg ttctagtcct ggcggaacac actgggggtg 2810

ggggcggggg aagatgcggt aatgaaaccg gttagtcaat tttgtcttaa tattgttgac 2870

aattctgtaa agttcctttt tatgaatatt tctgtttaag ctatttcacc tttcttttga 2930

aatccttccc ttttaaggag aaaatgtgac actttgtgaa aaagcttgta agaaagcccc 2990

tccctttttt ctttaaacct ttaaatgaca aatctaggta attaaggttg tgaattttta 3050

tttttgcttt gtttttaatg aacatttgtc tttcagaata ggattgtgtg ataatgttta 3110

aatggsaaaa acaaaacatg attttgtgca attaacaaag ctactgcaag gaaaataaaa 3170

cacttcttgg taacaaaaaa aaaaaaaaaa aa 3202

<210> 2

<211> 249
<212> PRT
<213> human

<400> 2

Met Ala Ala Val Ser Leu Arg Leu Gly Asp Leu Val Trp Gly Lys Leu
1   5   10   15

Gly Arg Tyr Pro Pro Trp Pro Gly Lys Ile Val Asn Pro Pro Lys Asp
            20   25   30

Leu Lys Lys Pro Arg Gly Lys Lys Cys Phe Phe Val Lys Phe Phe Gly
        35   40   45

Thr Glu Asp His Ala Trp Ile Lys Val Glu Gln Leu Lys Pro Tyr His
    50   55   60

Ala His Lys Glu Glu Met Ile Lys Ile Asn Lys Gly Lys Arg Phe Gln
65   70   75   80

Gln Ala Val Asp Ala Val Glu Glu Phe Leu Arg Arg Ala Lys Gly Lys
                85   90   95

Asp Gln Thr Ser Ser His Asn Ser Ser Asp Asp Lys Asn Arg Arg Asn
            100   105   110

Ser Ser Glu Glu Arg Ser Arg Pro Asn Ser Gly Asp Glu Lys Arg Lys
        115   120   125

Leu Ser Leu Ser Glu Gly Lys Val Lys Lys Asn Met Gly Glu Gly Lys
    130   135   140

Lys Arg Val Ser Ser Gly Ser Ser Glu Arg Gly Ser Lys Ser Pro Leu
145   150   155   160

Lys Arg Ala Gln Glu Gln Ser Pro Arg Lys Arg Gly Arg Pro Pro Lys
                165   170   175

Asp Glu Lys Asp Leu Thr Ile Pro Glu Ser Ser Thr Val Lys Gly Met
            180   185   190

Met Ala Gly Pro Met Ala Ala Phe Lys Trp Gln Pro Thr Ala Ser Glu
        195   200   205

Pro Val Lys Asp Ala Asp Pro His Phe His His Phe Leu Leu Ser Gln
    210   215   220

Thr Glu Lys Pro Ala Val Cys Tyr Gln Ala Ile Thr Lys Lys Leu Lys
225 230 235 240

Ile Cys Glu Asp Leu Leu Leu Pro Arg
245

<210> 3
<211> 34
<212> DNA
<213> human

<400> 3
acgtggatcc gcggctgtga gtctgcggct cggc 34

<210> 4
<211> 35
<212> DNA
<213> human

<400> 4
caacaagctt tcacctagga agaaggaggt cttca 35

<210> 5
<211> 41
<212> DNA
<213> human

<400> 5
acgaggatcc gccatcatgg cggctgtgag tctgcggctc g 41

<210> 6
<211> 36
<212> DNA
<213> human

<400> 6
gcatggtacc tcacctagga agaaggaggt cttcac 36

<210> 7
<211> 240
<212> PRT
<213> human

<400> 7

Met Ser Arg Ser Asn Arg Gln Lys Glu Tyr Lys Cys Gly Asp Leu Val
1 5 10 15

Phe Ala Lys Met Lys Gly Tyr Pro His Trp Pro Ala Arg Ile Asp Glu
20 25 30

Met Pro Glu Ala Ala Val Lys Ser Thr Ala Asn Lys Tyr Gln Val Phe

35 40 45

Phe Phe Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe
50 55 60

Pro Tyr Glu Glu Ser Lys Glu Lys Phe Gly Lys Pro Asn Lys Arg Lys
65 70 75 80

Gly Phe Ser Glu Gly Leu Trp Glu Ile Glu Asn Asn Pro Thr Val Lys
85 90 95

Ala Ser Gly Tyr Gln Ser Ser Gln Lys Lys Ser Cys Val Glu Glu Pro
100 105 110

Glu Pro Glu Pro Glu Ala Ala Glu Gly Asp Gly Asp Lys Lys Gly Asn
115 120 125

Ala Glu Gly Ser Ser Asp Glu Glu Gly Lys Leu Val Ile Asp Glu Pro
130 135 140

Ala Lys Glu Lys Asn Glu Lys Gly Ala Leu Lys Arg Arg Ala Gly Asp
145 150 155 160

Leu Leu Glu Asp Ser Pro Lys Arg Pro Lys Glu Ala Glu Asn Pro Glu
165 170 175

Gly Glu Glu Lys Glu Ala Ala Thr Leu Glu Val Glu Arg Pro Leu Pro
180 185 190

Met Glu Val Glu Lys Asn Ser Thr Pro Ser Glu Pro Gly Ser Gly Arg
195 200 205

Gly Pro Pro Gln Glu Glu Glu Glu Glu Glu Asp Glu Glu Glu Glu Ala
210 215 220

Thr Lys Glu Asp Ala Glu Ala Pro Gly Ile Arg Asp His Glu Ser Leu
225 230 235 240